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RAW SEQUENCE LISTING

DATE: 01/23/2002

PATENT APPLICATION: US/09/812,074

TIME: 10:03:22

Input Set : N:\Crf3\RULE60\09812074.raw.txt

Output Set: N:\CRF3\01232002\I812074.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Lester, Henry A.

6 Dascal, Nathan

7 Lim, Nancy

8 Schreibmayer, Wolfgang

9 Davidson, Norman

11 (ii) TITLE OF INVENTION: DNA ENCODING INWARD RECTIFIER, G-PROTEIN

12 ACTIVATED, MAMMALIAN POTASSIUM KGA

13 CHANNEL AND USES THEREOF

15 (iii) NUMBER OF SEQUENCES: 2

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP

19 (B) STREET: Four Embarcadero Center, Suite 3400

20 (C) CITY: San Francisco

21 (D) STATE: California

22 (E) COUNTRY: United States

23 (F) ZIP: 94111-4187

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/812,074

C--> 33 (B) FILING DATE: 19-Mar-2001

34 (C) CLASSIFICATION:

36 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/09/042,494

38 (B) FILING DATE:

40 (A) APPLICATION NUMBER: US 08/066,371

41 (B) FILING DATE: 21-MAR-1993

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Vance, Dolly A.

45 (B) REGISTRATION NUMBER: 39,054

46 (C) REFERENCE/DOCKET NUMBER: A-59891-1/RFT/DAV

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: (415) 781-1989

50 (B) TELEFAX: (415) 398-3249

51 (C) TELEX: 910 277299

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 2076 base pairs

ENTERED

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57      (B) TYPE: nucleic acid
58      (C) STRANDEDNESS: single
59      (D) TOPOLOGY: linear
61      (ii) MOLECULE TYPE: cDNA
63      (ix) FEATURE:
64          (A) NAME/KEY: CDS
65          (B) LOCATION: 32..1534
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA      52
70                                     Met Ser Ala Leu Arg Arg Lys
71                                     1           5
73 TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC      100
74 Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly
75      10           15           20
77 TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC      148
78 Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro
79      25           30           35
81 AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG      196
82 Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val
83      40           45           50           55
85 CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC      244
86 Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu
87      60           65           70
89 TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC      292
90 Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe
91      75           80           85
93 ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG      340
94 Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp
95      90           95           100
97 GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC      388
98 Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn
99      105          110          115
101 TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT      436
102 Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu
103 120          125          130          135
105 TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC      484
106 Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile
107      140          145          150
109 ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC      532
110 Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile
111      155          160          165
113 CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG      580
114 Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys
115      170          175          180
117 ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT      628
118 Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His
119      185          190          195
121 GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG      676
122 Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val

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123	200					205					210					215	
125	GGC	AAC	CTG	CGC	AAC	AGC	CAC	ATG	GTC	TCC	GCG	CAG	ATC	CGC	TGC	AAG	724
126	Gly	Asn	Leu	Arg	Asn	Ser	His	Met	Val	Ser	Ala	Gln	Ile	Arg	Cys	Lys	
127					220					225					230		
129	CTG	CTC	AAA	TCT	CGG	CAG	ACA	CCT	GAG	GGT	GAG	TTT	CTA	CCC	CTT	GAC	772
130	Leu	Leu	Lys	Ser	Arg	Gln	Thr	Pro	Glu	Gly	Glu	Phe	Leu	Pro	Leu	Asp	
131				235					240					245			
133	CAA	CTT	GAA	CTG	GAT	GTA	GGT	TTT	AGT	ACA	GGG	GCA	GAT	CAA	CTT	TTT	820
134	Gln	Leu	Glu	Leu	Asp	Val	Gly	Phe	Ser	Thr	Gly	Ala	Asp	Gln	Leu	Phe	
135			250					255					260				
137	CTT	GTG	TCC	CCT	CTC	ACC	ATT	TGC	CAC	GTG	ATC	GAT	GCC	AAA	AGC	CCC	868
138	Leu	Val	Ser	Pro	Leu	Thr	Ile	Cys	His	Val	Ile	Asp	Ala	Lys	Ser	Pro	
139		265					270					275					
141	TTT	TAT	GAC	CTA	TCC	CAG	CGA	AGC	ATG	CAA	ACT	GAA	CAG	TTC	GAG	GTG	916
142	Phe	Tyr	Asp	Leu	Ser	Gln	Arg	Ser	Met	Gln	Thr	Glu	Gln	Phe	Glu	Val	
143	280					285					290				295		
145	GTC	GTC	ATC	CTG	GAA	GGC	ATC	GTG	GAA	ACC	ACA	GGG	ATG	ACT	TGT	CAA	964
146	Val	Val	Ile	Leu	Glu	Gly	Ile	Val	Glu	Thr	Thr	Gly	Met	Thr	Cys	Gln	
147				300						305					310		
149	GCT	CGA	ACA	TCA	TAC	ACC	GAA	GAT	GAA	GTT	CTT	TGG	GGT	CAT	CGT	TTT	1012
150	Ala	Arg	Thr	Ser	Tyr	Thr	Glu	Asp	Glu	Val	Leu	Trp	Gly	His	Arg	Phe	
151				315					320					325			
153	TTC	CCT	GTA	ATT	TCT	TTA	GAA	GAA	GGA	TTC	TTT	AAA	GTC	GAT	TAC	TCC	1060
154	Phe	Pro	Val	Ile	Ser	Leu	Glu	Glu	Gly	Phe	Phe	Lys	Val	Asp	Tyr	Ser	
155			330					335					340				
157	CAG	TTC	CAT	GCA	ACC	TTT	GAA	GTC	CCC	ACC	CCT	CCG	TAC	AGT	GTG	AAA	1108
158	Gln	Phe	His	Ala	Thr	Phe	Glu	Val	Pro	Thr	Pro	Pro	Tyr	Ser	Val	Lys	
159		345				350					355						
161	GAG	CAG	GAA	GAA	ATG	CTT	CTC	ATG	TCT	TCC	CCT	TTA	ATA	GCA	CCA	GCC	1156
162	Glu	Gln	Glu	Glu	Met	Leu	Leu	Met	Ser	Ser	Pro	Leu	Ile	Ala	Pro	Ala	
163	360				365						370				375		
165	ATA	ACC	AAC	AGC	AAA	GAA	AGA	CAC	AAT	TCT	GTG	GAG	TGC	TTA	GAT	GGA	1204
166	Ile	Thr	Asn	Ser	Lys	Glu	Arg	His	Asn	Ser	Val	Glu	Cys	Leu	Asp	Gly	
167				380						385					390		
169	CTA	GAT	GAC	ATT	AGC	ACA	AAA	CTT	CCA	TCG	AAG	CTG	CAG	AAA	ATT	ACG	1252
170	Leu	Asp	Asp	Ile	Ser	Thr	Lys	Leu	Pro	Ser	Lys	Leu	Gln	Lys	Ile	Thr	
171				395					400					405			

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189 CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT      1492
190 Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn
191          475          480          485
193 CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA      1534
194 Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr
195          490          495          500
197 TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT CCAATATTTG      1594
199 GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT      1654
201 CAGAGGACTC TTCATTGAAG TGTGTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA      1714
203 TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT      1774
205 TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA      1834
207 AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT      1894
209 TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATAACATACA      1954
211 TACATGCATA TGCACAGACA CATAACACACA CATACTCATA TATATAAAAC ATACCCATAC      2014
213 AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCOA AAAAAAAAAA AAAAAACTCG      2074
215 AG      2076

(2) INFORMATION FOR SEQ ID NO: 2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
229 Met Ser Ala Leu Arg Arg Lys Phe Gly Asp Asp Tyr Gln Val Val Thr
230 1          5          10          15
232 Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly
233          20          25          30
235 Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp
236          35          40          45
238 Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr
239          50          55          60
241 Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp
242 65          70          75          80
244 Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu
245          85          90          95
247 Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu
248          100          105          110
250 Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr
251          115          120          125
254 Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile
255          130          135          140
257 Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile
258 145          150          155          160
260 Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu
261          165          170          175
263 Ile Gly Cys Met Phe Ile Lys Met Ser Gln Pro Lys Lys Arg Ala Glu
264          180          185          190
266 Thr Leu Met Phe Ser Glu His Ala Val Ile Ser Met Arg Asp Gly Lys
267          195          200          205

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269 Leu Thr Leu Met Phe Arg Val Gly Asn Leu Arg Asn Ser His Met Val
270      210      215      220
272 Ser Ala Gln Ile Arg Cys Lys Leu Leu Lys Ser Arg Gln Thr Pro Glu
273 225      230      235      240
275 Gly Glu Phe Leu Pro Leu Asp Gln Leu Glu Leu Asp Val Gly Phe Ser
276      245      250      255
278 Thr Gly Ala Asp Gln Leu Phe Leu Val Ser Pro Leu Thr Ile Cys His
279      260      265      270
281 Val Ile Asp Ala Lys Ser Pro Phe Tyr Asp Leu Ser Gln Arg Ser Met
282      275      280      285
284 Gln Thr Glu Gln Phe Glu Val Val Val Ile Leu Glu Gly Ile Val Glu
285      290      295      300
287 Thr Thr Gly Met Thr Cys Gln Ala Arg Thr Ser Tyr Thr Glu Asp Glu
288 305      310      315      320
290 Val Leu Trp Gly His Arg Phe Phe Pro Val Ile Ser Leu Glu Glu Gly
291      325      330      335
293 Phe Phe Lys Val Asp Tyr Ser Gln Phe His Ala Thr Phe Glu Val Pro
294      340      345      350
296 Thr Pro Pro Tyr Ser Val Lys Glu Glu Glu Met Leu Leu Met Ser
297      355      360      365
299 Ser Pro Leu Ile Ala Pro Ala Ile Thr Asn Ser Lys Glu Arg His Asn
300      370      375      380
302 Ser Val Glu Cys Leu Asp Gly Leu Asp Asp Ile Ser Thr Lys Leu Pro
303 385      390      395      400
305 Ser Lys Leu Gln Lys Ile Thr Gly Arg Glu Asp Phe Pro Lys Lys Leu
306      405      410      415
308 Leu Arg Met Ser Ser Thr Thr Ser Glu Lys Ala Tyr Ser Leu Gly Asp
309      420      425      430
311 Leu Pro Met Lys Leu Gln Arg Ile Ser Ser Val Pro Gly Asn Ser Glu
312      435      440      445
314 Glu Lys Leu Val Ser Lys Thr Thr Lys Met Leu Ser Asp Pro Met Ser
315      450      455      460
317 Gln Ser Val Ala Asp Leu Pro Pro Lys Leu Gln Lys Met Ala Gly Gly
318 465      470      475      480
320 Pro Thr Arg Met Glu Gly Asn Leu Pro Ala Lys Leu Arg Lys Met Asn
321      485      490      495
323 Ser Asp Arg Phe Thr
324      500

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VERIFICATION SUMMARY

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L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]